CLAIMS:

1. A method for synthesizing a peptide dimer, comprising:

(a) providing a linking moiety L_K having first and second functional groups capable of serving as initiation sites for peptide synthesis, and a third functional group attachable to a solid support;

(b) binding the linking moiety L_K to a solid support through the third functional group;

(c) synthesizing a first peptide segment at the first functional group and a second peptide segment at the second functional group, wherein each of said first and second peptide segments contain two cysteine residues positioned to allow intramolecular cyclization through a disulfide bond;

(d) oxidizing the compound provided in step (c) in a manner effective to promote formation of disulfide bonds between cysteine residues in the same peptide segment while minimizing formation of disulfide bonds between cysteine residues in different peptide segments.

2. The method of claim 1, wherein step (d) comprises treatment with an oxidizing composition containing an oxidizing reagent of a type and in an amount effective to minimize reaction products in which a cysteine residue of the first peptide segment binds to a cysteine residue of the second peptide segment.

3. The method of claim 2, wherein the oxidizing reagent is dimethyl sulfoxide.

4. The method of claim 3, wherein the oxidizing composition comprises approximately 15% to 100% (v/v) dimethyl sulfoxide.

5. The method of claim 4, wherein the oxidizing composition comprises approximately 50% to 100% (v/v) dimethyl sulfoxide.

6. The method of claim 5, wherein the oxidizing composition comprises approximately 50% to 100% (v/v) dimethyl sulfoxide.

7. The method of claim 6, wherein the oxidizing composition comprises approximately 80% to 100% (v/v) dimethyl sulfoxide.

8. The method of claim 7, wherein the oxidizing composition comprises approximately 100% (v/v) dimethyl sulfoxide.

9. The method of claim 1, wherein:

the first peptide segment is approximately 10 to 40 amino acid residues in length, binds to the erythropoietin receptor, and contains a sequence of amino acids $X_3X_4X_5GPX_6TX_7X_8X_9$ (SEQ ID NO: 1) wherein each amino acid is indicated by standard one-letter abbreviation, X_3 is C or homocysteine (Hoc), X_4 is R, H, L or W, X_5 is M, F, I or nor-leucine (J), X_6 is selected from any one of the 20 genetically coded L-amino acids and J, X_7 is W, 1-naphthylalanine (B) or 2-naphthylalanine (U), X_8 is D, E, I, L or V, and X_9 is C or Hoc; and

the second peptide segment is approximately 10 to 40 amino acid residues in length, binds to the erythropoietin receptor, and contains a sequence of amino acids $X'_3X'_4X'_5GPX'_6TX'_7X'_8X'_9$ (SEQ ID NO: 2) wherein each amino acid is indicated by standard one-letter abbreviation, X'_3 is C or Hoc, X'_4 is R, H, L or W, X'_5 is M, F, I or J, X'_6 is selected from any one of the 20 genetically coded L-amino acids and J, X'_7 is W, B or U, X_8' is D, E, I, L or V, and X'_9 is C or Hoc.